

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cerretti, Douglas P.
- (ii) TITLE OF INVENTION: Cytokine Designated as LERK-6
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: System 7.1
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US --to be assigned--
 - (B) FILING DATE:
 - (C) CLASSIFICATION:

- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2826

- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI SENSE: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: LERK-6

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCC CGG GCC AAC GCT GAC CGA TAC GCA GTC TAC TGG AAC CGT AGC AAC Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn 1 5 10 15	48
CCC AGG TTT CAG GTG AGC GCT GTG GGT GAT GGC GGC TAT ACC GTG Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Tyr Thr Val 20 25 30	96
GAG GTG AGC ATC AAC GAC TAC CTG GAT ATC TAC TGC CCA CAC TAC GGG Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly 35 40 45	144
GCG CCG CTG CCC CCG GCT GAG CGG ATG GAG CGG TAC ATC CTG TAC ATG Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met 50 55 60	192
GTG AAT GGT GAG GGC CAC GCC TCC TGT GAC CAC CGG CAG CGA GGC TTC Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe 65 70 75 80	240
AAG CGC TGG GAA TGC AAC CGG CCC GCA GCG CCC GGG GGA CCC CTC AAG Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys 85 90 95	288
TTC TCA GAG AAG TTC CAA CTC TIC ACC GCG TIF PIF STG GCG TTT GAG Phe Ser Glu Lys Phe Glu Leu Phe Thr Pro Phe Ser Leu Gly Phe Gln 100 105 110	336
TTC CGG CCT GGC CAC GAA TAC TAC TAC ATC TCT GGC ACA CCT CCC AAC Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn 115 120 125	384
CTC GTG GAC CGA CCC TGC CTG CGA CTC AA; GTT TAT GTG CGT CCA ACC Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr 130 135 140	432
AAT GAG ACC CTG TAT GAG GGT CCA GAG CCC ATC TTC ACC AGT AAC AGC Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser 145 150 155 160	480
TCC TGC AGC CGC CTG GGT GGC TAC GAC CTC TTC CTC ACC ACC GTC CCT Ser Cys Ser Gly Ile Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro 165 170 175	528
GTG CTG TGG TCC CTI CTG GGC TAC TAG Val Leu Ile Ser Ile Leu Ile Val Pro 180	555

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
 1 5 10 15

Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
 20 25 30

Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
 35 40 45

Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
 50 55 60

Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
 65 70 75 80

Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
 85 90 95

Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
 100 105 110

Phe Arg Pro Gly His Glu Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
 115 120 125

Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
 130 135 140

Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
 145 150 155 160

Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
 165 170 175

Val Leu Trp Ser Leu Leu Gly Ser
 180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATATTTACT GCCCGCACTA CAACAGCT

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAGAAGGCG CTGTAGCGCT GGAAC

25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACGTAGTCTA CTGGAACTCC AGTAACCCCA G

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCCTCAAGC ACTGGCCAGA ACTCTCTCTG GAGT

34

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

G TTC CAC GCA GGC GCG GGG GAC GAC GGC GGG GGC TAC ACG GTG GAG Phe His Ala Gly Ala Gly Asp Asp Gly Gly Gly Tyr Thr Val Glu 1 5 10 15	46
GTG AGC ATC AAT GAC TAC CTG GAC ATC TAC TGC CCG CAC TAT GGG GCG Val Ser Ile Asn Asp Tyr Leu Asn Ile Tyr Cys Pro His Tyr Gly Ala 20 25 30	94
CCG CTG CCG CCG GCC GAG CGC ATG GAG CAC TAC GTG CTG TAC ATG GTC Pro Leu Pro Pro Ala Glu Arg Met Glu His Tyr Val Leu Tyr Met Val 35 40 45	142
AAC GGC GAG GGC CAC GCC TCC TGC GAC CAC CGC CAG CGC GGC TTC AAG Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe Lys 50 55 60	190
CGC TGG GAG TGC AAC CCG CCC GCG GCG CCC GGG GGG CCG CTC AAG TTC Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys Phe 65 70 75	238
TCG GAG AAG TTC CAG CTC TTC ACG CCC TTC TCC CTG GGC TTC GAG TTC Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe 80 85 90 95	286
CGG CCC GGC CAC GAG TAT TAC TAC ATC T Arg Pro Gly His Glu Tyr Tyr Tyr Ile 100	314

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe His Ala Gly Ala Gly Asp Asp Gly Gly Gly Tyr Thr Val Glu Val
1 5 10 15

Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly Ala Pro
20 25 30

Leu Pro Pro Ala Glu Arg Met Glu His Tyr Val Leu Tyr Met Val Asn
35 40 45

Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe Lys Arg
50 55 60

Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys Phe Ser
65 70 75 80

Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Arg
85 90 95

Pro Gly His Glu Tyr Tyr Tyr Ile
100